

BEST AVAILABLE COPY

WO 2005/080426

PCT/GB2005/000572

1/12

MAAAASPAFLRLPLLLLSSWCRTGLADPHSLCYDITVIPKIRPGPRWCAVQGQVDE
KTFLHYDCGSKRTPVSPLEGKKLNVTAWKAQNPVLREVVDILTEQLLDIQLENYIP
KEPLTLQARMSCEQKAEGHGSGSWQPSFDGQIFLLFDSQNRMWTTHPGPRKMKEKW
ENDKDMTMSFHYISMGDCTGWLEDFLMGMDSTLEPSAGAPPTMFGTAQPRATATT
ILCCLLIMCLLICSRHSLTQSHGHHPQSLQPPPHPPLLHPTWLLRRVLWSDSYQIAK
RPLSGGHVTRVTLPIIGDDSHSLPCPLALYTINNGAARYSEPLQVSIS

Figure 1

MAAAASPAFLRLPLLLLSSWCRTGLADPHSLCYDITVIPKIRPGPRWCAVQGQVDE
KTFLHYDCGSKRTPVSPLEGKKLNVTAWKAQNPVLREVVDILTEQLLDIQLENYIP
KEPLTLQARMSCEQKAEGHGSGSWQPSFDGQIFLLFDSQNRMWTTHPGPRKMKEKW
ENDKDMTMSFHYISMGDCTGWLEDFLMGMDSTLEPSAGGT

Figure 2

2/12

1 cctgcgagcc gccaggtgat ccacgggctg ggcttcgctt ctgctgtccc ctgcgatcca
61 actccccaaat ggcagcggcc gccagccccg cgttccttct acgcctcccg cttctgctcc
121 tgctgtccag ctggtgcaagg accgggctgg ccgaccctca ctctcttgc tatgacatca
181 ccgtcatccc taagttcaga cctggaccac ggtggtgtgc ggttcaaggc caggtggatg
241 aaaagacttt tcttcactat gactgtggca gcaagacagt cacacccgtc agtcccctgg
301 ggaagaaaact aaatgtcaca acggcctgga aagcacagaa cccagtaactg agagaggtgg
361 tggacatact tacagagcaa ctgcttgaca ttcagctgga gaattacata cccaaggaac
421 ccctcaccct gcaggccagg atgtcttgc agcagaaagc cgaaggacac ggcagtggat
481 cttggcagct cagttcgat ggacagatct tcctcctctt tgactcagaa aacagaatgt
541 ggacaacggt tcatcctgga gccagaaaga tgaaagaaaa gtgggagaat gacaaggata
601 tgaccatgtc cttccattac atctcaatgg gagactgcac aggatggctt gaggacttct
661 tcatggccat ggacagcacc ctggagccaa gtgcaggagc accacccacc atgtcctcag
721 gcacagccca acccagggcc acggccacca ccctcatcct ttgctgcctc ctcatcatgt
781 gtctcctcat atgctccagg cacagtctga cccaaagcca tggccaccac ctcagtc
841 tgcagcctcc tcctcatcct cccctgcttc atcctacctg gctgctgaga agagtc
901 ggagtgacag ctaccaaata gcgaagcgcc cttgtctgg tggacacgtg actcgctgt
961 ctttacctat cattggagac gactcacact ctttaccctg ccctcttgcc ttgtatacaa
1021 taaataacgg cgccagg tattcggagc cactcaggc tccatatctt gatggttccc
1081 tggcccccagc tgtctttct tccgtcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1141 aaa

Figure 3

3/12

1 atggcagcg ccgccagccc cgcgttcctt ctacgcctcc cgttctgct cctgctgtcc
61 agctggtca ggaccgggct ggccgaccct cactctctt gctatgacat caccgtcatc
121 cctaagttca gacctggacc acggtgtgt gcggttcaag gccaggtgga tgaaaagact
181 tttcttcact atgactgtgg cagcaagaca gtcacacccg tcagtcctt gggaaagaaa
241 ctaaatgtca caacggcctg gaaagcacag aacccagtac tgagagaggt ggtggacata
301 cttacagagc aactgcttga cattcagctg gagaattaca tacccaagga acccctcacc
361 ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtgg atcttggcag
421 ctcagttcg atggacagat cttcctcctc tttgacttag aaaacagaat gtggacaacg
481 gttcatcctg gagccagaaa gatgaaagaa aagtggaga atgacaagga tatgaccatg
541 tccttcatt acatctcaat gggagactgc acaggatggc ttgaggactt cttgatggc
601 atggacagca ccctggagcc aagtgcagga ggcacagtct gacccaaagc catggccacc
661 accctcagtc cctgcagcct cctcctcatt ctccctgtct tcattctacc tggctgctga
721 ggagagtctt ttggagtgtac agtacccaa tagcgaagcg ccccttgtct ggtggacacg
781 tgactcgcgt gactttaccc atcattggag acgactcaca ctccttaccc tgccctcttgc
841 cttgtatac aataaataac ggcgcagcca ggtattcgga gccactacag gtctccatat
901 cttgatggtt ccctggcccc agctgtctt tcttcgtc

Figure 4

4/12

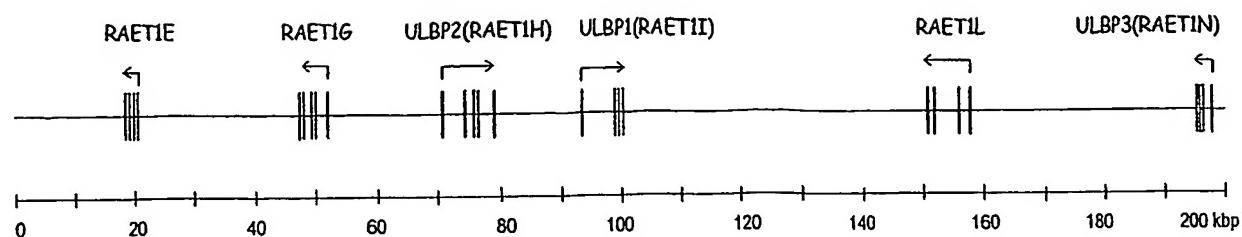


Figure 5

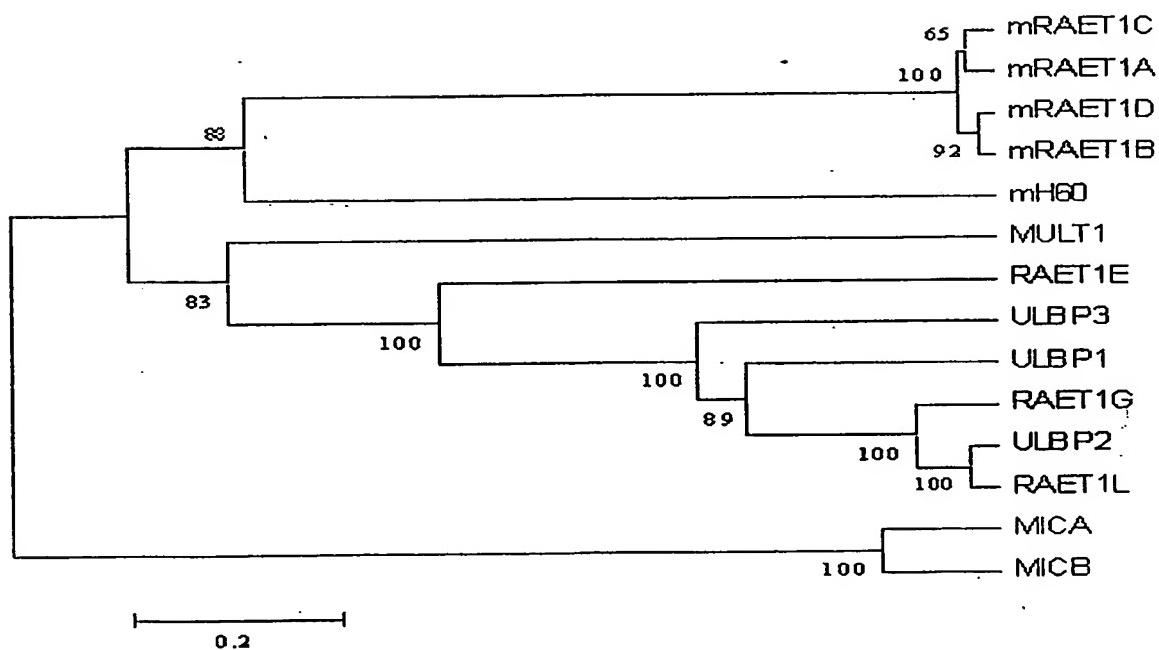


Figure 6

Raet1g
ulbp2
Raet1e
ulbp3

-MAAAASPAFLRLPLL-LISSLWCRTGLADPHSLCYDITVICKRPGPRWCAVQGQVDEK 58
-MAAAATKILLCLPLL-LIISGWSRAGRADPHSLCYDITVICKFRRPGPRWCAVQGQVDEK 59
-MRRISLTSPVRLLFLILLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKN 59
-MAAAASPAILPRLAILPPLLFDWSGTGRADAHSLWYNFTIIHLPRHQQWCEVQSQVDQK 60

Raet1g
ulbp2
Raet1e
ulbp3

TELYHYDCGSKRVTPVSPLGKKLNVTAWKAONPVLREVVVDILTEQLLDIQLENYIPKEPL 118
TELYHYDCGNKTVTPVSPLGKKLNVTAWKAONPVLREVVVDILTEQLRDIQLENYTPKEPL 119
LFLQYNSDNNDNNMVVKPLGLGKVNATSTWGEITOTLGEVGRDIRMLLCDIKPQIKTS-DPS 118
NFLSYDCGSDRVLKGHLEEQLYATDAWGKQLEMILREVGORLRLIELADTEILEDFTPSGPL 120

Raet1g
ulbp2
Raet1e
ulbp3

TLQARMSCEQKAEGHGSGSMQPSFDGQIFLFDSQNRMWTTTHPGPRKMKEKWENDKIDMT 178
TLQARMSCEQKAEGHSSGSWQFSFDGQIFLFDSEKRMMWTTVHPGARKMKEKWENDKVVA 179
TLQVEMFCQHEAERCTGASWQFTINGEKSLLFDAMNMWTVINHEASKIKETWKDRGLE 178
TLQVRMSCECEADGYIRGSWQFSFDGRKFLLFDSSNNRKWTWVHAGARRMKEKWEKDSGLT 180

[Raet1g alternative splice ending]
Raet1g
ulbp2
Raet1e
ulbp3

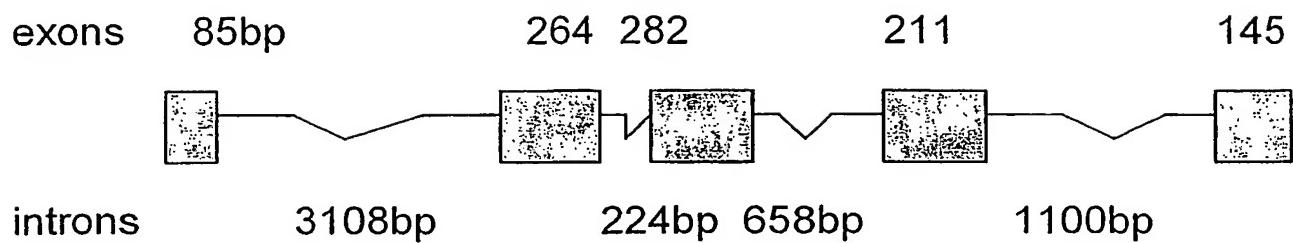
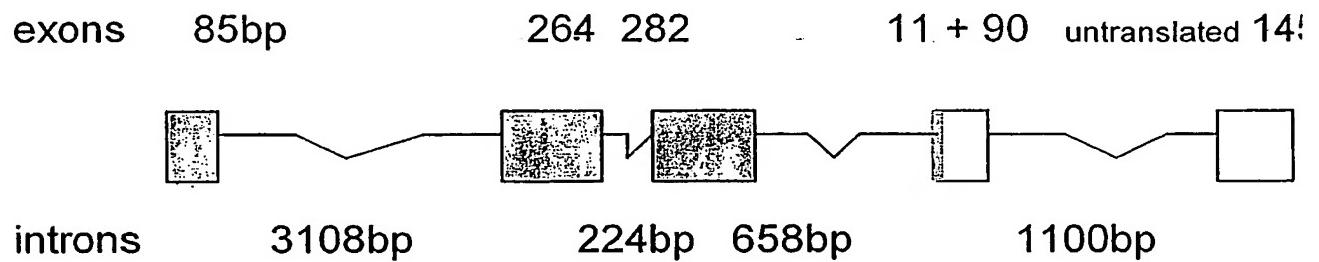
SAGGTV
MSFHYISMGDCIGWIEDFLMGMDSTLEPSAGAPPTMFSGTAQPRATATTLLICCLIMCI 238
MSFHYFSMGMDCIGWIEDFLMGMDSTLEPSAGAPLAMSSGGTQLRATATTLLICCLIL-- 238
KYFRKLSKGDCDHWLREFLGHWEAMPEPTVSPVNASSDIHWSSSSLPDRWIIIGAFILLVL 238
TEFKMVSMDCKSWIIRDFLMHRKKRLEPTA--PPTMAPGLAQPKAIATTLLSPWSELILIL-- 237

Raet1g
ulbp2
Raet1e
ulbp3

LICSRHSLTQSHGHHPQSLQOPPPHPPPLLHPTWLLRVLWSDSYQIAKRPPLSGGHVTRVT 297
PCFILPGI----- 246
MGIVLICVWWONGEWQAGLWPLRTS----- 263
CFILPGI----- 244

Raet1g
LPIIGDDSHSLPCPLALYTIINNGAARYSEPIQVSIIS 333

Figure 7

RAET1G**RAET1G2****Figure 8**

7/12

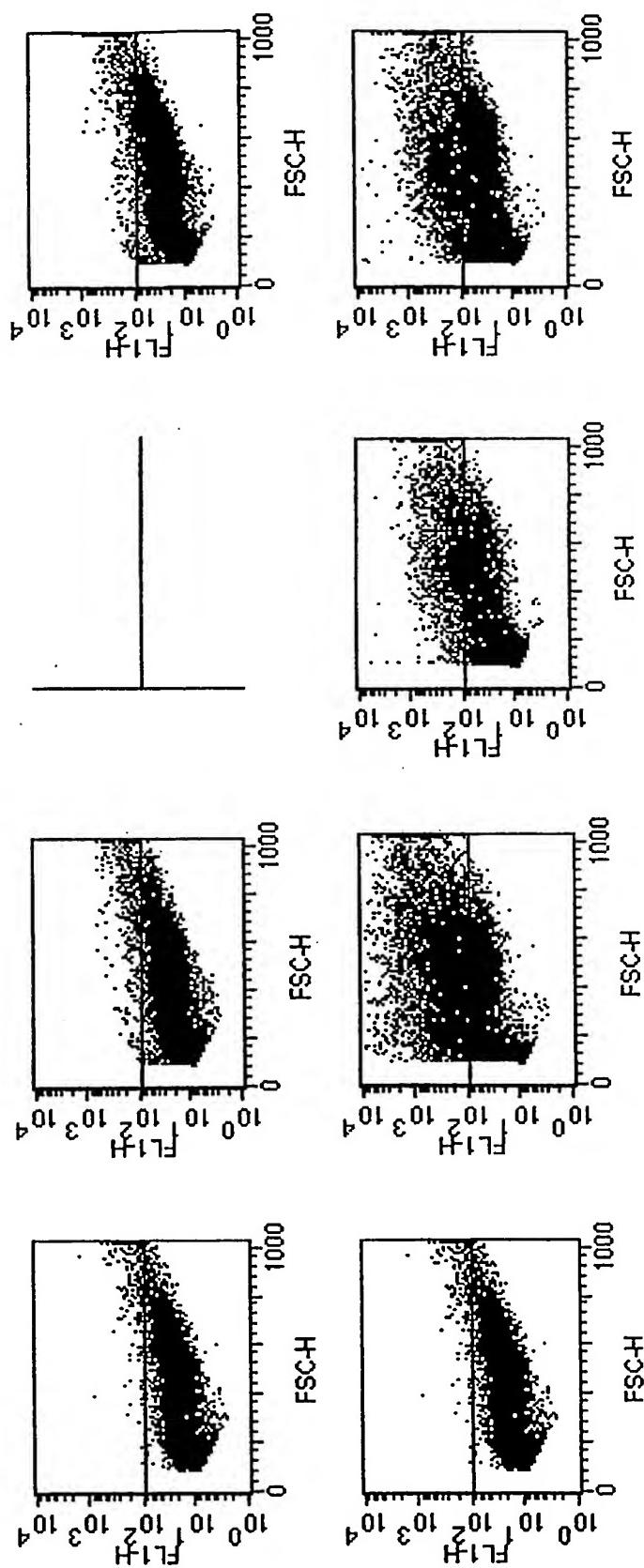


Figure 9

8/12

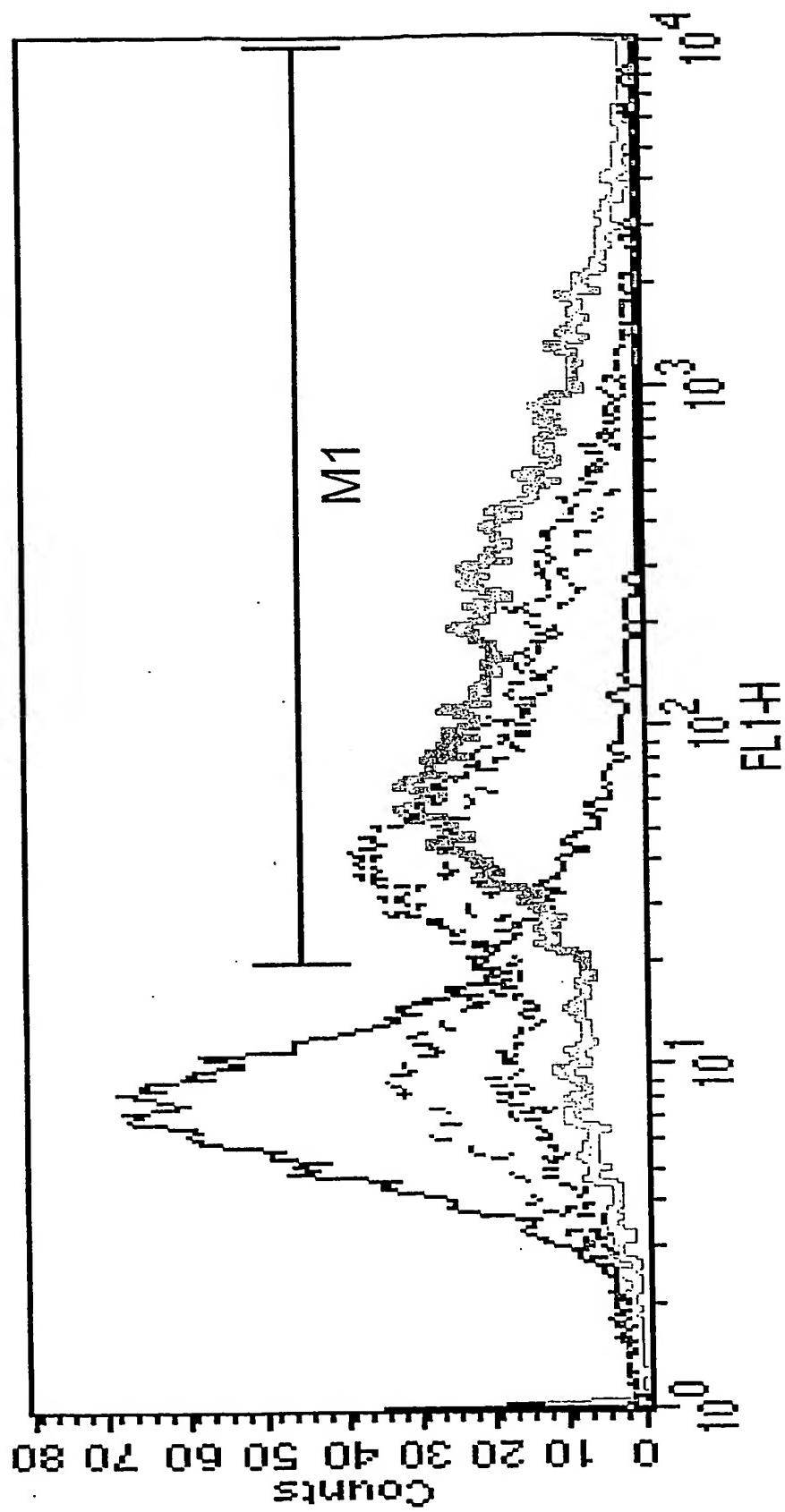


Figure 10.

9/12

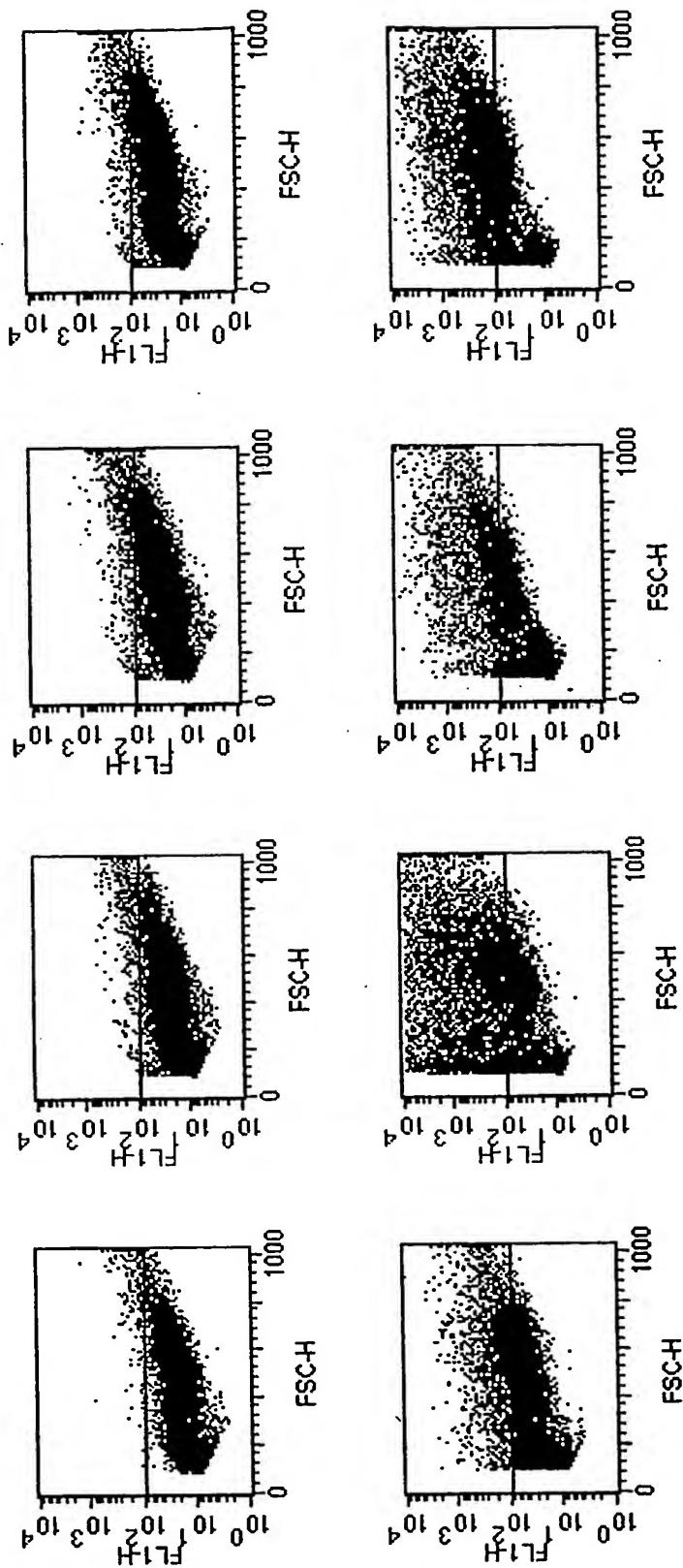


Figure 11

9/12

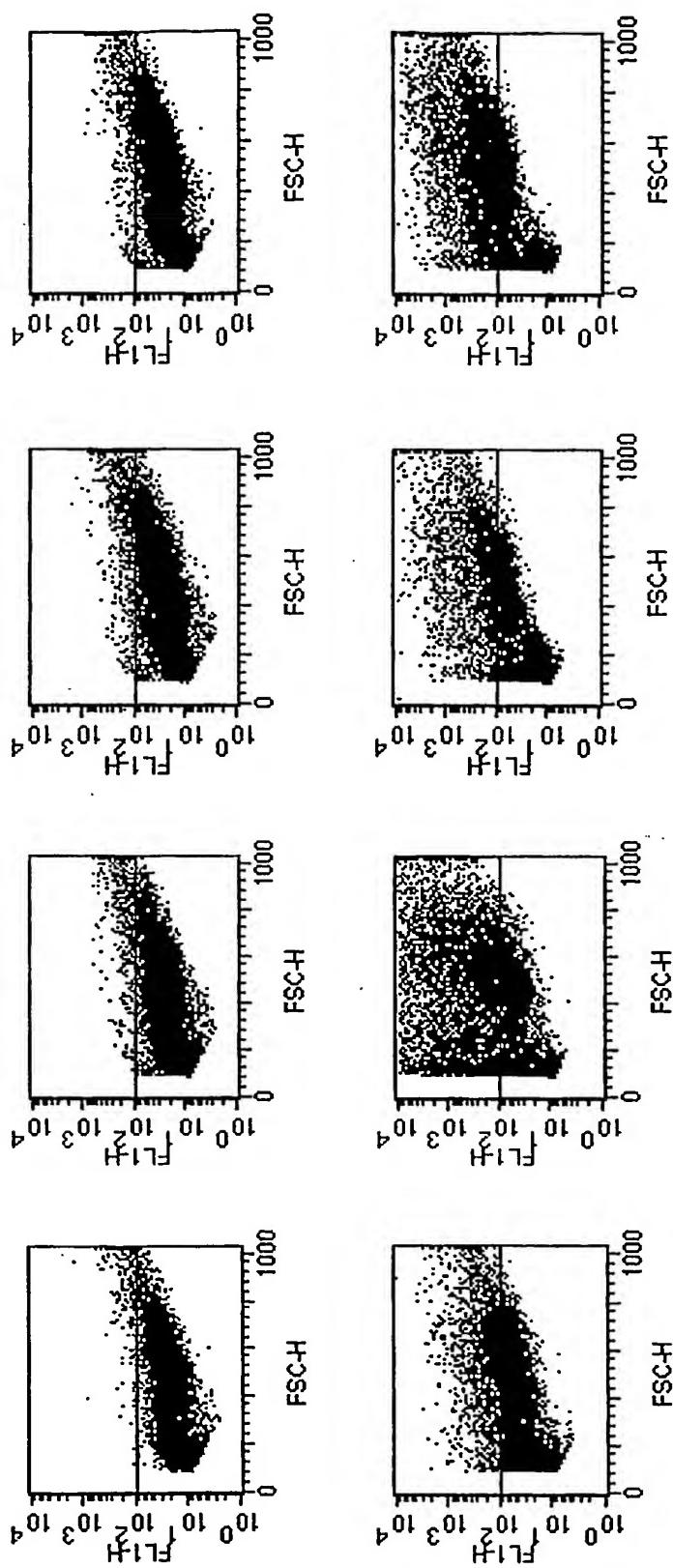


Figure 11

10/12

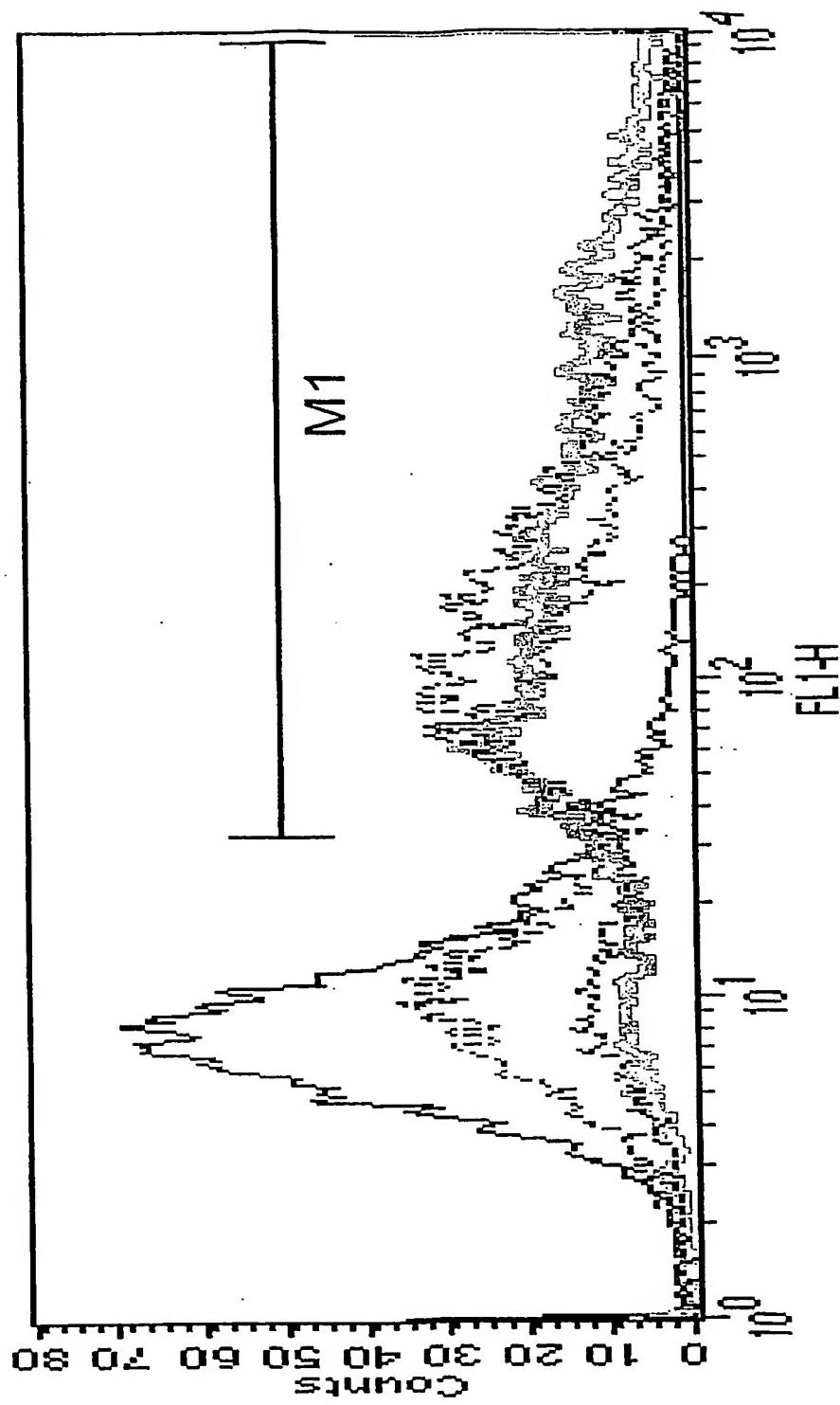


Figure 12

11/12

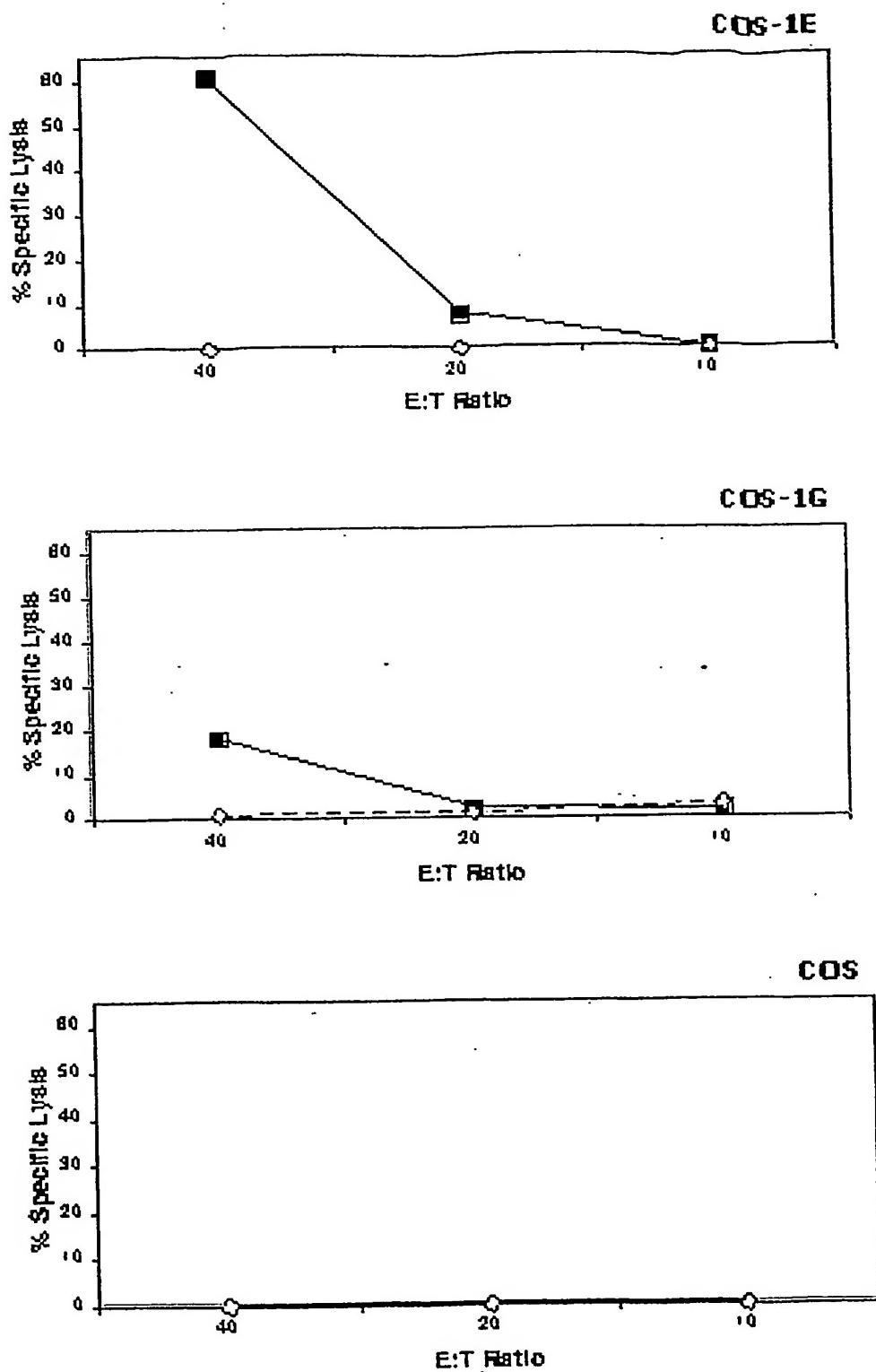


Figure 13

12/12

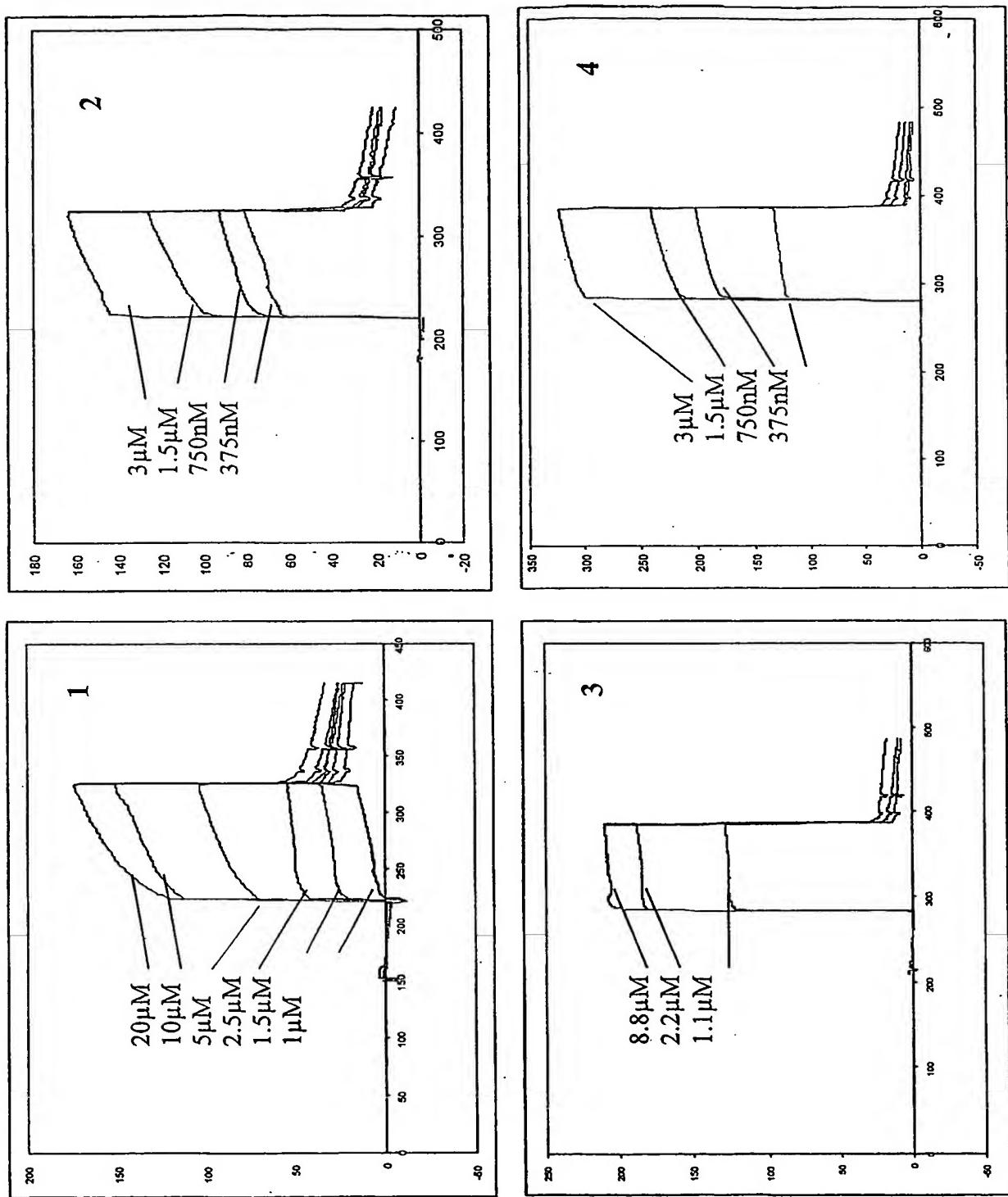


Figure 14